

Fig. 1

Target 5'---3' (SEQ ID NO:)	Binding-helix amino acids at positions -1 1 2 3 4 5 6	Specificity
GAA (1)	Q S S N L V R	GAA (GAT)
(17)	Q R S N L V R	GAA, GAT
(18)	Q S G N L V R	GAN
(19)	Q P G N L V R	GAN
GAC (2)	D P G N L V R	GAC
(20)	D P G N L K R	GAC, GAT
GAG (3)	R S D N L V R	GAG
(21)	R S D N L R R	GAG, GGG
(22)	K S A N L V R	GAG, (GAT)
(23)	R S D N L V K	GAG, (GGG)
(24)	K S A Q L V R	UNSPEC.
GAT (4)	T S G N L V R	GAT
GCA (5)	Q S G D L R R	GCA, GCT
(25)	Q S S T L V R	GTA, GCA
(26)	Q S G T L R R	GTA, GCA/T/C
(27)	Q P G D L V R	GCT, GCC, GCA

Fig. 1

	(28)	Q G P D L V R	GCT, GCA
	(29)	Q A G T L M R	GTA, GCA
	(30)	Q P G T L V R	GTA, GCA
	(31)	Q G P E L V R	non-binder
GCC	(6)	D C R D L A R	GCC
	(32)	G C R E L S R	GCC
	(33)	D P S T L K R	GCC (GCA/T GTC)
	(34)	D P S D L K R	GCC, GAC
	(35)	D S G D L V R	GCC, GAC
	(36)	D S G E L V R	GCT, GCC
	(37)	D S G E L K R	GCT, GCC, GTC
GCG	(7)	R S D D L V K	GCG
	(38)	R L D T L G R	GNG
	(39)	R P G D L V R	GCG, GNG, GCN
	(40)	R S D T L V R	NG
	(41)	K S A D L K R	GAG, GTG, GCT, GCC
	(42)	R S D D L V R	GAG, (GNG, GCN)
	(43)	R S D T L V K	GNG

Fig. 1

	(44)	K S A E L K R	GCT, GCC, UNSPEC.
	(45)	K S A E L V R	GCT, GCC, UNSPEC.
	(46)	R G P E L V R	UNSPEC.
	(47)	K P G E L V R	NON-BINDER, BUT EXPR.
GCT	(8)	T S G E L V R	GCT
	(48)	S S Q T L T R	GCT
	(49)	T P G E L V R	GCT
	(50)	T S G D L V R	GCT, (GCC, GCA)
	(51)	S S Q T L V R	GCT
	(52)	T S Q T L T R	GCT (GAT, GTC, GCC)
	(53)	T S G E L K R	GCT, GCC
	(54)	Q S S D L V R	GCT (GCA, GCC)
	(55)	S S G T L V R	GCC, GCT
	(56)	T P G T L V R	GCT, GTC
	(57)	T S Q D L K R	GCC, GCT
	(58)	T S G T L V R	GCT, UNSPEC.
GGA	(9)	Q R A H L E R	GGA
	(59)	Q S S H L V R	GGA
	(60)	Q S G H L V R	GGA

Fig. 1

	(61)	Q P G H L V R	GGA, GCT
GGC	(10)	D P G H L V R	GGC
	(62)	E R S K L A R	GGC
	(63)	D P G H L A R	GGC
	(64)	Q R A K L E R	GGC
	(65)	Q S S K L V R	GGC
	(66)	D R S K L A R	GGC, GGN
	(67)	D P G K L A R	GGC, unspec.
GGG	(11)	R S D K L V R	GGG
	(68)	R S D K L T R	GGG
	(69)	R S D H L T R	GGG, GAG
	(70)	K S A K L E R	NON-BINDER
GGT	(12)	T S G H L V R	GGT, GCA
	(71)	T A D H L S R	GGT, GAT
	(72)	T A D K L S R	GGG, (GGT)
	(73)	T P G H L V R	GGT, unspec.
	(74)	T S S H L V R	unspec.
	(75)	T S G K L V R	unspec.
GTA	(13)	Q S S S L V R	
	(76)	Q P G E L V R	GTA, (GCT)
	(77)	Q S G E L V R	GTA, GCA/C

Fig. 1

	(78)	Q S G E L R R	GTA, GCA/T/C
GTC	(14)	D P G A L V R	
	(79)	D P G S L V R	GTC (GCT, GCC)
GTC	(15)	R S D E L V R	GTG, (GAG, GCG)
	(80)	R K D S L V R	GTG, GNG
	(81)	R S D V L V R	GTG, GAG, GGG
	(82)	R H D S L L R	GTG, GAG, GNG
	(83)	R S D A L V R	GAG, GTG, GGG
	(84)	R S S S L V R	GTG
	(85)	R S S S H V R	GTG, GGG
	(86)	R S D E L V K	GTG
	(87)	R S D A L V K	GAG GTG GGG
	(88)	R S D V L V K	GAG GNG
	(89)	R S S A L V R	GNG
	(90)	R K D S L V K	GGG GNG
	(91)	R S A S L V R	GAG, unspec.
	(92)	R S D S L V R	GCT unspec.
	(93)	R I H S L V R	unspec.

Fig. 1

	(94)	R P G S L V R	UNSPEC.
	(95)	R G P S L V R	UNSPEC.
	(96)	R P G A L V R	UNSPEC.
	(97)	K S A S L V R	NON-BINDER
	(98)	K S A A L V R	NON-BINDER
	(99)	K S A V L V R	NON-BINDER
GTT	(16)	T S G S L V R	GTT, GCT
	(100)	T S G S L T R	GGT, GCT
	(101)	T S Q S L V R	GAT, GTA GCT, GCA
	(102)	T S S S L V R	GTA, GAT
	(103)	T P G S L V R	GTA
	(104)	T S G A L V R	GGT, GCT, GAT
	(105)	T P G A L V R	GGT, GAT, GCT
	(106)	T G G S L V R	GGT, GAT
	(107)	T S G E L V R	GCT GCG GTA GTT
	(108)	T S G E L T R	GCT GTA/T/C
	(109)	T S S A L V K	UNSPEC
	(110)	T S S A L V R	UNSPEC

A

-30	erbB-2	-1	
AGCCAT	GGGGCCGGAGCCGCAGTG	AGCACC	SEQ ID NO: 123
GCAAT	CGGAGCCGGAGCCGGAGTCC	GGGGA	SEQ ID NO: 124
-135	erbB-3	-164	

B

	10	20	30	40	
E2C	MAQA	LEPGEKPYACPECGKSFS	SRKDSLVR	HQRTHTGEKP	
E3	MAQA	LEPGEKPYACPECGKSFS	SDPGALVR	HQRTHTGEKP	
	50	60	70	80	
E2C	YKCPECGKSFS	QSGDLRRH	HQRTHTGEKPYK	CPECGKSFS	SD
E3	YKCPECGKSFS	QSSHLVR	HQRTHTGEKPYK	CPECGKSFS	SD
	90	100	110	120	
E2C	CRDLAR	HQRTHTGEKPYACPECGKSFS	QSSHLVR	HQRTHT	
E3	CRDLAR	HQRTHTGEKPYACPECGKSFS	QSSHLVR	HQRTHT	
	130	140	150	160	
E2C	GEKPYKCPECGKSFS	SDCRDLAR	HQRTHTGEKPYKCPECGK		
E3	GEKPYKCPECGKSFS	SDCRDLAR	HQRTHTGEKPYKCPECGK		
	170	180			
E2C	SFSRSDKLVR	HQRTHTGKKTSGQAG		SEQ ID NO: 125	
E3	SFSQSSHLVR	HQRTHTGKKTSGQAG		SEQ ID NO: 126	

Fig. 2